AMENDMENTS TO THE CLAIMS

The following list of claims will replace all prior versions and lists of claims in the application.

Listing of Claims:

1.   (Currently amended) A method <u>for diagnosis of renal cell carcinoma (RCC)</u>, <u>the method</u> comprising the steps of:

providing at least one peripheral blood sample of a human; and

comparing an expression profile of one or more <u>RCC disease </u>genes in said at least one peripheral blood sample to at least one reference expression profile of said one or more <u>RCC disease </u>genes, wherein <u>the difference or similarity between the expression profile and the at least one reference</u> <u>expression profile of said one or more RCC disease genes is indicative of the presence or</u> <u>absence of RCC in the human,</u> ~~each of said one or more genes is differentially expressed in~~ ~~peripheral blood mononuclear cells (PBMCs) of patients having a solid tumor as compared to~~ ~~PBMCs of disease-free humans,~~ and wherein said one or more <u>RCC disease </u>genes include at least one gene selected from Table 4 or Table 6, provided that if said one or more <u>RCC disease</u> genes consist of only one gene, said one gene is not selected from the group consisting of IL1B, IL6, MMP-9 and FCGR3B, and further provided that if said one or more <u>RCC disease </u>genes consist of two genes, said two genes are not IL1B and IL6.

2.   (Canceled)

3.   (Currently amended) The method according to claim 1<u>2</u>, wherein said peripheral blood sample comprises enriched <u>peripheral blood mononuclear cells </u>(PBMCs<u>)</u>.

4.   (Currently amended) The method according to claim 1<u>2</u>, wherein[[,]] said peripheral blood sample is a whole blood sample.

5.   (Currently amended) The method according to claim 1<u>2</u>, wherein the expression profile is determined using quantitative RT-PCR or an immunoassay.

6.   (Currently amended) The method according to claim 1, wherein said at least one reference expression profile comprises an expression profile of said one or more <u>RCC disease</u> genes in peripheral blood samples of disease-free humans.

7.   (Currently amended) The method according to claim 6, wherein said at least one reference expression profile further comprises an expression profile of said one or more <u>RCC disease</u> genes in peripheral blood samples of patients having <u>RCC</u>said solid tumor.

8.   (Currently amended) The method according to claim 7, wherein said one or more <u>RCC disease</u> genes include at least two genes, and the expression profile of the human is compared to said at least one reference expression profile using a weighted voting algorithm.

9-11.   (Canceled)

12.   (Currently amended) The method according to claim 1, wherein said one or more <u>RCC disease</u> genes include at least one gene which has an RNA transcript capable of hybridizing under stringent conditions to a classification probe sequence (CPS) selected from Table 2.

13.   (Currently amended) The method according to claim 1, wherein said one or more <u>RCC disease</u> genes include at least one gene which has an RNA transcript capable of hybridizing under stringent conditions to a qualifier selected from Attachment A.

14.   (Withdrawn-currently amended) The method according to claim 1, wherein said one or more <u>RCC disease</u> genes include at least two genes selected from Table 4.

15.   (Currently amended) The method according to claim 1, wherein said one or more <u>RCC disease</u> genes include a classifier identifiable using a two-class or multi-class correlation metric algorithm.

16-20. (Canceled)